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Fig. 1

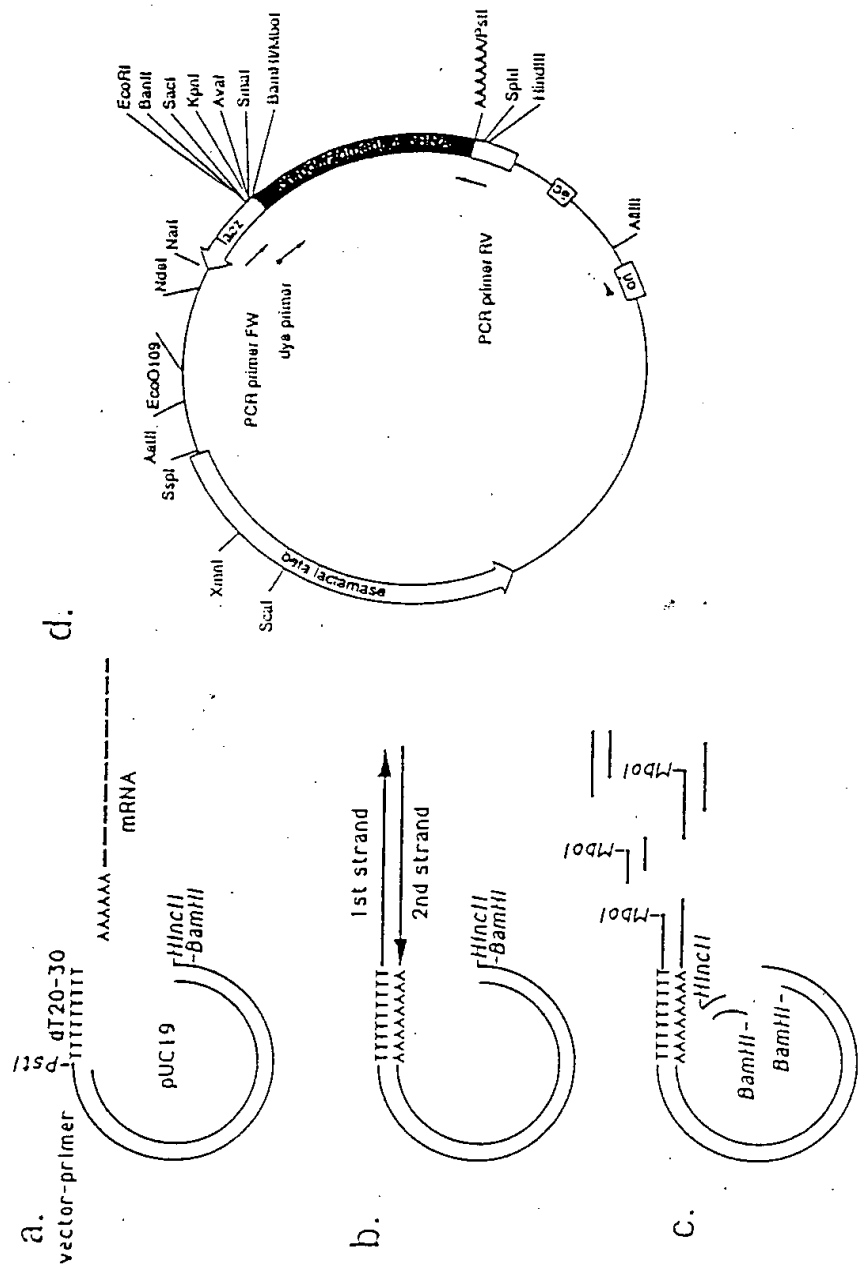
a.
vector-primer
dT20-30
pUC19
mRNA
AAAAA
HincII
BamHI
b.
1st strand
2nd strand
c.
BamHI
HincII
d.
EcoRI
BanII
SacI
KpnI
AvaI
SmaI
AAAAAA/PstI
SphI
HindIII
AatII
lacZ
NdeI
NaeI
PCR primer FW
Uye primer
PCR primer RV
EcoO109
AatII
SspI
XmnI
ScaI
Orfa lactamase

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Fig. 2

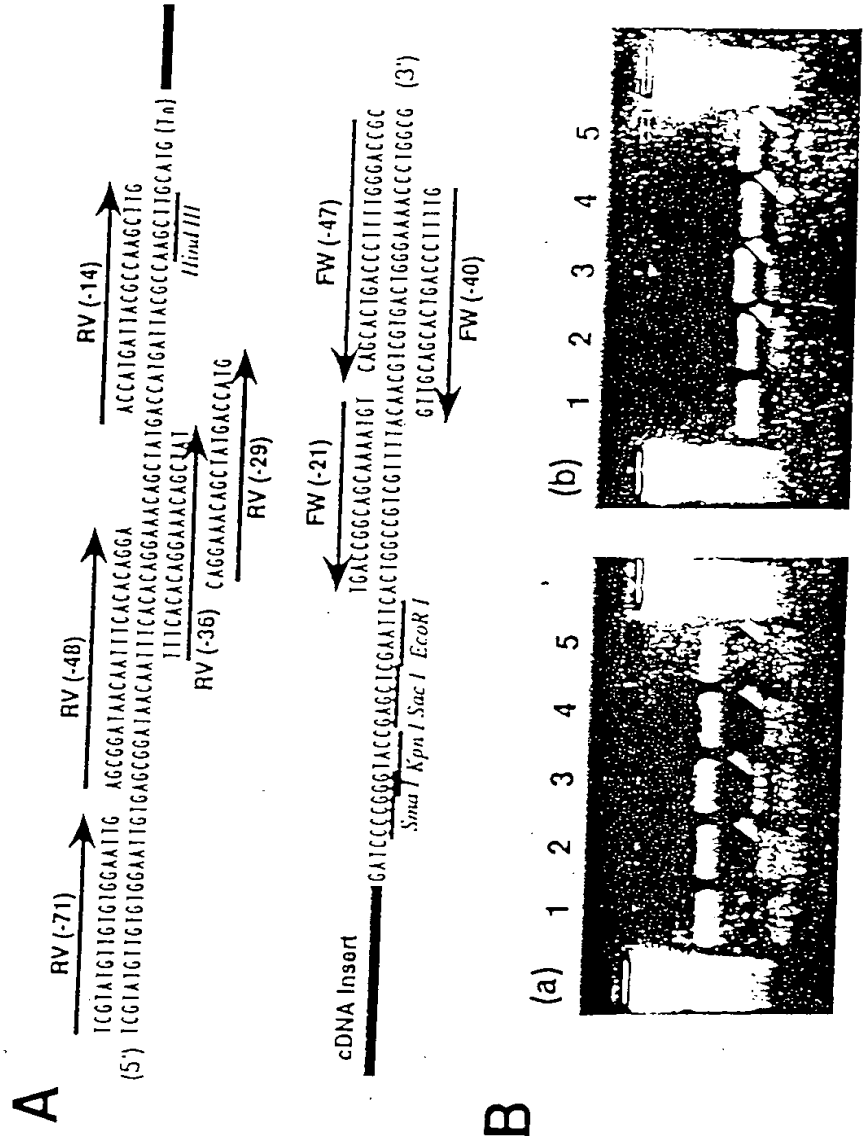

Fig. 3

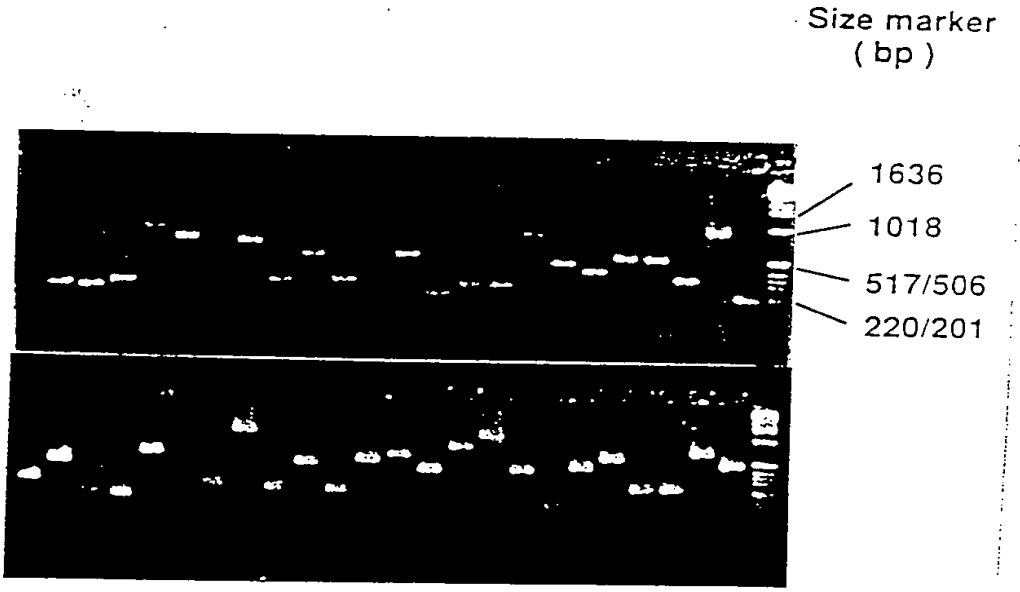

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Fig. 4

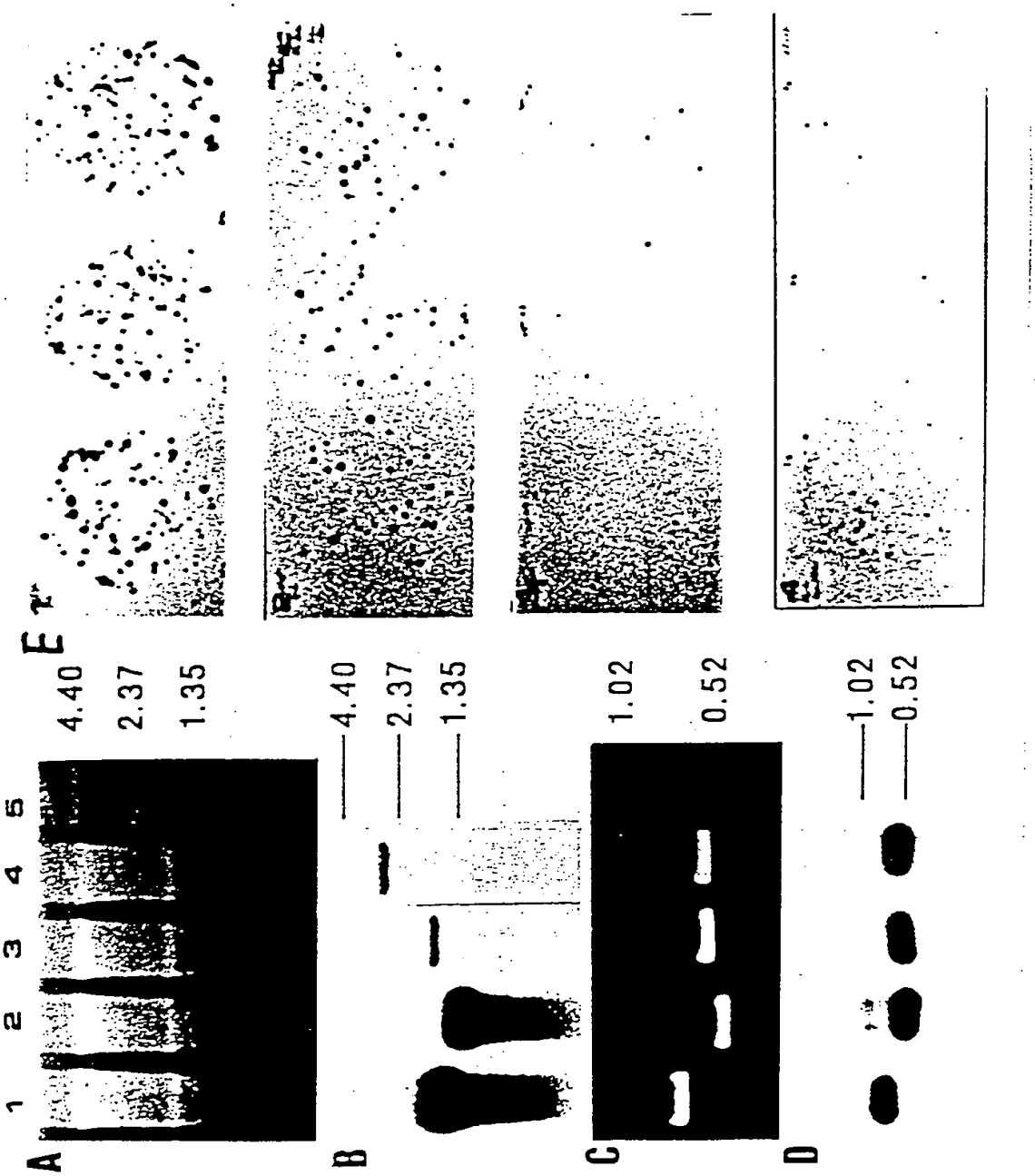

Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1-α	α1-antitrypsin	HnRNP core protein A1	Inter-α-trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b)Band intensity of control blot(cpm)	133	177	100	127
(c)Normalized signal(a)/(b)x10	52	24	1	1.2
(d)Positive signals on colony blot	307	119	7	9
(e)Relative representation	44	17	1	1.3

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library

Group	Clone	Gene	A in 982 (%)	B "in 8,800 (%)"	C "in 26,400 (%)"
I	a15	Elongation factor - 1Aα	22 (2.2)	307 (3.5)	NT
	c321	Translationally restricted tumor protein	12 (1.2)	89 (1.0)	NT
	lb038	α-1-antitrypsin	8 (0.8)	119 (1.4)	NT
	hm01b02	Light chain of ferritin	6 (0.6)	62 (0.7)	NT
	c13a04	NADP(H) Menadione oxidoreductase	4 (0.4)	27 (0.3)	NT
	hm02d02	Ribosomal protein S11	3 (0.3)	29 (0.3)	NT
	lb042	Human RNP core protein A1	2 (0.2)	7 (0.1)	NT
II	s155	unknown	1	2	5 (0.02)
	s159	unknown	1	2	4 (0.02)
	s639	unknown	1	1	3 (0.01)
	s635	unknown	1	0	2 (0.01)
	s170	unknown	1	0	1 (0.004)
	s154	unknown	1	0	1 (0.004)
	s167	unknown	1	0	1 (0.004)
	s645	unknown	1	0	1 (0.004)
	s647	unknown	1	0	0 (<0.004)
	s632	unknown	1	0	0 (<0.004)

Fig. 5

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Fig. 6

GS	Cit	Chromosomal position	Sequences of primers		AT	HO	HE	HO	CO	G	T	
			Sense	Anti-sense								
gs0007aa	pm2366	1	CAGAGCCCCAGTACAACTAT	AAGTTTATTGTTGGGGTCAG	48	114	115	104	110	1	2	
gs0001026	pm2444	1	AATGGGACAGTTACACTTGA	CCAGCTTCCTTGACTTGAGA	48	83	81	>200	>200	1	1	
gs0001075	pm0883	1	TGGACTGTGGATACCTATCT	ACAAGTACCCCTGAATGGCT	48	124	124	103	107	4	4	
gs0001087	pm1772	1	GTCACTCTCAGCCATAGCAC	ACCATCTTCAGCCCACACTT	50	104	104	180	>200	6	6	
gs0001094	pm0347	1	GCCCCTAACACGAGGAACTC	TAATTTCCCACTCCCGTAAC	51	114	116	>200	200	1	1	
gs0001116	pm1771	1	GGGTTTTCAATAGGGTGTAGACC	GCCCCAATGTGTCAAAACTG	49	95	95	78	107	1	1	
gs0001191	pm0609	1	TTGCTGGATTGTAACTTTTG	GGCTGAACATTCACTCTTTG	47	97	97	-	200	1	1	
gs0001200	pm1351	1	TTAAGAAGACCCTTATGGAGACC	AATAATCTTGGTTAGTCACTTAC	47	97	98	-	-	1	1	
gs0001346	pm0982	1	TCAGGTCTGCTTGGAGGATG	AACTCACAGCACAGTATTTG	53	120	122	>200	>200	1	1	
gs0001446	pm1518	1	AAGGTGTACAGGATATTTGCAGA	TGCAATAGCCCAATCTCATT	47	130	125	>200	>200	1	1	
gs0001464	pm1439	1	CCAAAGACCTCCGTTGAACA	TTTGGGAGAGCCATAGACAG	51	100	100	>200	-	1	1	
gs0001468	pm0427	1	TACTCAGTGGAAAGATAAAC	CAGTGGACCACATTTTCTTA	40	98	98	-	-	2	2	
gs0001521	pm2785	1	CCCAAATCAAATTGTTAAATG	TTTGAATCAGAGACATGAAGTT	43	102,175	100	>200	>200	1	1	
gs0001554	pm2291	1	CCAGAGAGTTCAAGGGATTG	GGTACAAAGTGCAAATGACT	46	57	57	78	155	1	1	
gs0001572	pm2006	1	CCAACATGGTCCTAGCACTG	AAACTTTATTGCAGCTTCTT	44	58	59	>200	>200	4	4	
gs0001720	pm1950	2	CATGATACTCTTCGGTGGTA	AAACAGTAGTTGCCAGCATT	46	84	103	-	-	1	1	
gs0001806	pm1730	2	AGGCTGAAATGTGGCATGCT	CCCGTTATTGCTACATGTCT	48	119	119	93	115	1	1	
gs0001881	pm0931	2	AAAGCAATACAAAATACCAA	TTCAATATGTTTAACCAGTA	40	90	90	-	-	1	1	
gs0001890	pm0925	2	TAATGTACCACGATGAATAG	TAATGTAATAATGCAGGTAA	45	88	88	-	-	1	1	
gs0001213	pm2010	2	CCAGATGGAAAGGGAAGTCT	CTGGAATATGGAGAATCAAACAG	47	125	125	150	>200	1	1	
gs0001252	pm0935	2	TCGAGTTTTGTCTCTAATAA	GGAAATAATCGCTTCAGTTG	43	103	103	-	-	1	1	
gs0001268	pm2093	2	AGTCCTTCTTGGCTCCTCAT	TATCGTCAGTGCCTTTATTG	52	137	137	>200	-	1	1	
gs0001438	pm2435	2	TTTTGTACCTACGTAAGAGTACTT	ATCCGTGCCACACATAGTGA	45	105	108	-	-	1	2	
gs0001442	pm1671	2	TTATTAGGGAGTCATTATTCTGTG	AGTTCCCATTCTTCCACATG	45	67	65	>200	>200	1	2	
gs0001453	pm1245	2	TTGCTTTCCCGTCTCTAAGT	ATGTACAATTTGCGTATGTAGG	45	75	75	170	190	1	1	
gs0001535	pm1246	2	ATCTACTGTTTGTTGAAGTG	ACTGATTTTGGTCCCATCTG	44	68	67	-	-	1	1	
gs0000875	pm0449	3	CGAACATTTCACCTCTCATA	ATGATTTATTTAGGCAGGAA	43	68	68	-	-	3	6	
gs0001001	pm1758	3	TCTGGCTCTTTGGTGTTGGA	GGCCCACTGAGTACAATGTC	51	115	115	-	-	1	1	
gs0001218	pm2434	3	AAAGAAAGCACACTGCCTAA	ATGTATAGACAAATCCAAAG	42	90	90	-	-	1	1	
gs0001219	pm0668	3	GTAGTCTCCTGCCCTTTAGC	AAGGATTTGATTTTCTACAT	43	77	77	-	-	1	1	
gs0001277	pm1729	3	GGTCCTGTTTATTTTGACAT	AAACAAGAGGATGGTTCAGA	43	75	75	155	>200	1	1	
gs0001306	pm1022	3	GATCCTTGGTGTGTAGTTCAGTC	CTGCAAAATACAGGGAATCAT	46	83	83	160	140	1	1	
gs0001418	pm2209	3	ACCCCAGTCCCAAATCCAGT	ACACTCCCCCAGCCCTTACT	55	105	105	113	>200	1	1	
gs0001466	pm2455	3	ATCTAGCTGGCTGTAGTATT	TTAAAGAGATGAATTTATTGGT	42	130	130	190	>200	1	1	
gs0000271	pm1252	4	GTCCTTTGCTATCTGTGTTA	AAGCATTTATTTGAGGTTTA	43	90	90	95	>200	1	3	

Fig. 7

gi|000448	pm2256	4	GGCCAAGTTTCTTCTAGTAT	GTTCAGTTTTATTCAGAGCA	42	62	62	>200	69	1	2	
gi|001052	pm1151	4	GTGCCATGCACTGTTGTTAT	GTCATATATTCCATCATCAA	43	80	80	.	.	1	1	
gi|001215	pm0988	4	AGAAAATTAATAGCATAGGT	TAGAGTCAAAGTTGCCTGTG	43	100	100	130	.	1	1	
gi|001298	pm2367	4	ATCAAAGTTTAATTGCTTCA	CATCCCATCACATACAAGTC	43	116	116	>200	180	1	1	
gi|000993	pm0904	5	TCTCGTGAAGAGCAGCACAA	TCTAAAGGAAGAACAGCATC	49	101	102	113	200	1	1	
gi|000938	pm1889	5	AAGCAATGCCTTATCCACAG	CTAAAGAGCTTGAACCCTTCAT	45	87	87	>200	>200	1	1	
gi|001065	pm0019	5	TCACCCAGATAATTTACAGT	GAGACATAAGCAGGTAAGAT	44	120	120	.	.	1	1	
gi|001101	pm2364	5	TTACCTTACCGTGTCTTTAC	AGACAAATATCCCAAAAAGC	47	89	89	190	>200	1	1	
gi|001461	pm1160	5	ATTTTGTGAGTGGTTTACTA	AGAAATGGATGCTTTTATTC	43	101	99	>200	>200	1	1	
gi|000053	pm2720	6	AATGTCATAGTCTCCTTTCA	TGCATCCTTCAATGTCTTCT	44	78	78	72	>200	2	3	
gi|001326	pm1154	6	CATTGAGACAGCAGCAACAG	CCTGGCCCTCTTCCTGAGTA	53	102	104	145	200	1	1	
gi|001434	pm1216	6	TAGGCAAAACACGAGAAGAG	AAGGAGCTGGTGTCAGGTTC	48	65	65	110	>200	1	1	
gi|001457	pm1785	6	TATATGCAAATATTCCAAAGTCTG	TCTAATAATTCTGGTCCCTTATCT	46	90,>200	90	>200	>200	1	1	
gi|001523	pm0285	6	TTGTAACGTGTGTCGTCAGT	TTTAAAAATGTCATGGTAAT	42	86	70	>200	100	1	1	
gi|001525	pm0328	6	GCACCTAAGCCTCCCAAAGT	TTTTATATCAGTCCAAGAGC	49	138	138	>200	>200	1	1	
gi|001562	pm2619	6	TCTGCATTGACAAGGACCAC	TTTGAGATTTTAATGAGTCATTC	43	62	62	>200	45	1	1	
gi|000624	pm0991	7	GACCTGAAGTGTGAATGAGT	AACTTAGCTTTATGGGATTT	45	119	119	>200	.	1	2	
gi|001145	pm0281	7	AGCCAAACTCGGGGTCATCT	CCACGGGACAGGTGAGTCAT	56	159	159	115	>200	4	4	
gi|001469	pm0219	7	AATCATTTGGCGAGACTGTA	AAGACAACTTTATCCAGACA	45	88	88	130	.	1	1	
gi|001579	pm1102	7	TCAGGCAGTCTGCTCAGATA	TTTGCAGGTTAATCTGTTTA	44	77	76	170	.	1	1	
gi|001207	pm0956	8	AACAGTATTGCGTTGTCAGACTAG	TCCATTAATAAGGCCAGTCTTCAG	47	81	81	105	70	1	1	
gi|001176	pm2527	9	TTGCCTCTAATGGTGTCTAC	AAAAACCAGAACACACTAAG	48	99	99	118	180	1	1	
gi|001248	pm2708	9	TGTATTGGATTTGGATTCTC	CAAAAGCAAAACAGCAGATA	44	95	95	.	85	1	1	
gi|000260	pm0995	97	TTGCCATCAAACACATACA	CTTGTGAGTTTTGGTTTCTG	43	55	55	.	.	1	1	
gi|001055	pm0959	97	TTAAAGAATCACCCTCATTG	CACATGCTTATTGGAACACT	44	74	74	72	73	1	1	
gi|001157	pm0547	10	AAGTATTGTGCAAAGATGTA	AAGAAAACACTGCCTTGTGG	45	138	139	>200	>200	2	3	
gi|001258	pm2245	10	TGTGAAATGCTATCTCTCCT	GCAATCGTTTCCATATCAGT	47	100	100	200	>200	1	1	
gi|000328	pm2664	11	ATCAAAACAAACAATCCAGA	ACTATAATATACTGCCAACT	42	117	121	134	95	2	2	
gi|001159	pm0880	11	GAATAGCTTGGAGATTTCAC	GGAGAATCATACCTTCAGCA	46	100	100	84	95	1	1	
gi|001315	pm0445	11	AAAGTGACCTTGATGGACAGTGGA	TCGAGCCAAAAATACATGCTGACT	50	153	153	>200	160	1	2	
gi|001352	pm2943	11	AGGGTGAAGGGTATTTTACG	CACATCATGGTTGAGAGCTA	47	83	85	.	.	2	2	
gi|001469	pm0559	11	AACCCTCTAGTAAGGCATTG	TTATTAAACCAAATCCAGTA	37	47	47	125	53	1	1	
gi|001570	pm2810	11	CTGTAAAGGTTTTTGGAATTATGT	TTTCATTTTTCTACCAGATTTATT	42	75,82	75	145	>200	3	3	
gi|000279	pm0266	12	AGTGTATGGAAGACCTTGAG	GTTCATTGAAACGGTGTAGC	48	130	130	101	>200	1	2	
gi|001163	pm2756	12	TCTCCCTATTCACAACCAGT	AATGATTTCGTAGGATAGCA	49	88	83	>200	120	1	2	
gi|001193	pm1193	12	CACAGCATAAAAGAATCATA	ACCCTAATTTAGTTTCTCAC	46	100	100	.	.	1	1	
gi|001235	pm2790	12	CATCATGGTACAGTCAGAAG	CAGTTTGTCAAAATGTATTG	44	83	82	93	87	1	1	
gi|001274	pm1355	12	AGATGTCAGTATTCTCCTCATGG	GAGAACAGCAGTAAAGCAACCAC	47	87	87	>200	>200	1	1	
gi|001308	pm0368	12	CCAAAGTGCTAGGGTTACAG	TTCAATAGACCTTGGGTTAC	47	95,165	95	>200	>200	1	1	
gi|000159	pm2645	13	CTAAGATTTAATGCGATTCC	AGTTAGTGTATGGCAGAGGA	46	104	104	>200	.	1	2	

gs001044	pm1659	13	TTGTAAGCCTATCAGAGTCA	AGACAGACTTATGCCATCTA	44	109,200	109	>200	100	1	1
gs001290	pm1731	13	GCTTCTTCCTGTGCTGTGGT	GCAGTTAATCATGGCTATTCTCC	50	122	122	>200	190	1	1
gs001362	pm0118	13	ACTGAAATGGAACATAGTCT	TACATTACATGACATTGTGA	40	61	61	95	103	1	1
gs001366	pm0364	13	TGCTTAGCTTTCCCTCCTTA	GAGCATTTCTGTTGTTCCTA	45	67	67	-	-	1	1
gs001389	pm2301	13	CATGAACCTGCTCACGACAA	GCCTTACTTTAATGCTGACC	51	100	100	100,>200	-	1	1
gs001492	pm0541	13	AAATGAATGTAAATAGCACT	ATTTAGTTTACAGGGAGAAT	41	72	72	-	74	1	1
gs001367	pm0441	14	GTTTTAAGTTTTGATTTGGG	CATTCCACTCTTACATTTCT	41	77	77	>200	180	3	4
gs001564	pm2307	14	CGTTCCTAAACTCTGAAATC	AATGCTCATTTATTCTCAAG	42	55	55	>200	>200	1	1
gs001576	pm2019	14	ATCACAATTACCTTTAGTTG	ACGATAACTTTATTGGAGAT	39	69	69	-	-	1	1
gs001339	pm2220	15	TCCCCATCCTCAGTTGAAGT	TGAGAACAAAAGGAACCAGT	47	70	70	80	150	1	1
gs000980	pm0985	16	TTGGAATGGAACCCTTGCTA	ACTTATGCTGCCTGAAATGG	48	79	79	66	70	2	2
gs001242	pm1127	16	CCCTTGTTTTTACATGTTCA	TATTAAATTCTCCCATTCAT	44	105	105	103	102	2	2
gs001516	pm2543	16	ACAGTGCTAAAATCAAAGGTG	TCTGACAACTCAAGGTGCAAT	45	70	70	>200	-	1	1
gs001566	pm0913	16	TTTGTGTCGGACTATGTAAT	TCACTTTTAATGGGAACCAG	41	53	53	>200	>200	1	1
gs000806	pm1157	17	CTCTCCATGTTCTCTACAAG	TAGAAGGAGAATCTGTGGTT	47	77	77	140	>200	2	3
gs001015	pm2369	17	ATATTCACCTTCCCATCCAT	TCAAATACGTCCTCTCAAGC	50	80	80	>200	>200	1	1
gs001156	pm0202	17	CAGAAATTAAGTGCAGCAAT	TCGTATCTGCATCTTTAAGT	45	103	100	>200	>200	2	2
gs001173	pm2117	17	AAAATCTTGTGGTTATTTCC	GTGATTCTACTGTACATTGC	41	118	118	145	200	1	1
gs001301	pm1878	17	TAAATTTGTGGAAATCTCTTGGA	ACACATTTGGGTTTGCTTTAAC	47	100	100	95	97	1	1
gs001316	pm0511	17	TGTGACAGCAGCAGCTTCAT	TCGTACATTTTAATTCCACC	45	128	129	-	1	1	1
gs001356	pm0538	17	CATCTCACAGACAAGGAAAC	ACCTAAGAGTCCAGAGAAAC	48	90	90	69	>200	1	1
gs001495	pm2212	17	TGACTGCAATAAGGAGTTGT	GAACATACCACGTTTATTTCT	46	90	90	180	>200	1	1
gs001522	pm0642	17	GTCTTCAGCAGATTTCAGGT	ACTTTCTTCTTGAGGACACA	45	68	68	160	-	1	1
gs001078	pm1815	19	TGTGTTCTCCAGCTTTGTAG	GTTACATTGCCTTGGTACAG	48	65	65	>200	>200	1	1
gs001417	pm0289	19	GGATCAGACCAACAGTGCTG	GCAAGGTATAAAACAGATTA	46	90	90	-	-	1	1
gs001467	pm1688	19	GAAGCCCACCCTGCACCTCA	GGAGAGTATTGGGGAACGGT	54	93	93	>200	>200	2	2
gs001069	pm1879	20	GCCATGCTTGTAAAGTGATGT	TTAAGAAGCCATTAGCTAGGATA	48	140	140	-	-	1	1
gs001068	pm1146	20	GCCCTTAGGATTCACTGCTC	ACCACCCAAGGTCTTTCAGG	52	66	66	180	>200	1	1
gs001089	pm0112	20	TGCTGGATGACTTCTACACG	TCCCTATCATGGCTGCTGTT	49	59	59	59,115	59	1	1
gs001128	pm0332	20	CTGCTCGGCTAGTCTGACTC	CAAATGGTCTAAGAGGACAT	49	135	135	153	160	1	1
gs001132	pm0647	20	TCTGAATGATGATGGAAACA	ATCCTAGTCCCAACCCAGTA	48	109	109	-	-	1	1
gs001158	pm1774	20	GGAGCCACATGGATTGATTG	AAATGTACCCCTGGCACCTC	52	124	124	>200	>200	1	1
gs001210	pm1235	20	AGCCATCTGGTTATGTCTTA	GGAGCAGAATGAAACTTCAC	44	90	90	>200	>200	1	1
gs001377	pm1701	20	TCCATGGTGTTAGAAGCCAG	CCACATCTCCAACAGGGAGT	54	142	142	>200	74	1	1
gs001395	pm2101	21	GTCAGCTCAATGCTACACAG	TTTATAGTGCAACACAGAGT	45	130	130	180	>200	1	2
gs001427	pm0648	21	CTTCTGCTATAAAAGTAGAG	ACAATTGGTTCACTAAATGA	39	58	58	145	>200	1	1
gs000978	pm0912	22	GGTGTAGTGTAACCATTTAG	AGTTGCACCCATCTCCTGTC	46	124	124	>200	>200	1	1
gs001444	pm0911	22	GGTCTTGTTCTCCCATCTGT	AGAAAGCCCCAAAGTAGTCC	48	65,88	65	100	125	1	2
gs001473	pm2231	22	TGAGCTGCACTTACCTGTGAGAG	AAGCAGGTTGAGTTGGGTTTTCT	50	94	94	67	135	2	4
gs001479	pm2328	22	TACAGCCCTCCCAGCTAAAC	TTTATTCTGCATCCACTACAA	46	65	65	190	>200	1	1

Fig. 8

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gs000999	pm1759	X	CTGCCATAGTTACCTGGATT	TCACCCACCACTATTTAGCA	47	103	103	-	-	1	1
gs001149	pm2180	X	GGAGGGGAGATATAGATTGT	AAAAAAATCCAGAAGACTGA	46	70	70	135	150	1	1
gs001161	pm0608	X	TTCTATAAGTGTGACCAGTT	GGAGGATTTGAGATACACAT	40	85	85	>200	77	1	1
gs001406	pm1294	X	TAATGCCAGTGAATGTTGCGTAA	GTAAAGGTTTATCCTTGCATCAGA	47	82	82	>200	80	2	3
gs001168	pm2289	1,18	ATCCTGCTGAAATACATCTG	GGGGAGAGACATCACATGAC	46	70	70	68	130	1	1
gs001436	pm0113	1,2,12,13,Y	GATCCGATGGGAGTGTAAAT	AATACAAAGCTAAACCACAA	44	69	69	170	-	1	1
gs001404	pm2272	1,2,3,5,8,12,14,17,X	TTGGAATTGACATTCTCTAT	TTTATTGTAACAAAGCAACT	43	130	130	150	132	2	2
gs000803	pm0314	1,2,6,X	TATCAAGCTGAAAATGTCAC	TTACTGAATCCAGCCAACCA	45	93	93	110	-	1	3
gs000140	pm1461	1,3,4,5,8,16	TCCAAATGAAGAAGGTGTTA	AGTTGACAGCCAGGTGAATG	49	96	96	100	100	1	3
gs001354	pm1561	2,20,21,22	GTCTGTCAAGCCAAGATTCA	TTTTTATTGTTGCTCCAAGT	48	110	110	170	150	1	1
gs000336	pm2795	2,4,5,10,12,15,17,20,22,Y	GACCTGTGACATTCTGGACT	TTATATGGTTGTTACACTCG	43	61	61	-	-	2	6
gs001077	pm0943	2,5,14,C	GCCTTGTTATTTCACCACTC	ATCTCCCTTTGCTCCAGTTA	46	82	82	>200	82	1	1
gs001192	pm1853	2,8,12	TCTGAGGACATTCCAAGACAG	CAGTCAAAACCAACACGGTAT	49	95	95	93	160	1	1
gs000213	pm1778	2,9,13,17,X	TGCAATAAAGGGAAAGACCA	CCGTTGTAGGTGATGAAATG	49	78	80	>200	>200	1	2
gs000919	pm0885	20,X	GTCATTTGTATGCAATTTCC	ACATTTTTATTTTTTCAACG	37	45	45	-	-	1	2
gs001109	pm0457	3,10,15	CATGTACTCAGAGGCACTTC	GCAACTACAAATCCCAAACT	50	133	133	>200	150	2	2
gs000071	pm2651	3,4,M	CAGGGACTGGAGCAGGAAAG	GATTTAACCCATTAGGAAGC	50	101	101	101	88	3	3
gs001426	pm2632	3,6	TTAGGAAAATATGGTTAGACAG	ATAGTATTGGGTTGACACAGTA	43	80	80	>200	120	1	1
gs001391	pm1133	3,8	TGGATTTGCTTTACCTTGTT	ACACCCTCAGGAGATGTTAC	47	93	93	95	>200	1	1
gs000077	pm2258	3,9,10,15	GCACTACAAGCCAAATCAGA	CTTCTTAACACCAACAGCAG	50	96	96	>200	125	2	10
gs000605	pm0628	4,6	GGATTTCTATTTGCTGTCAT	GTTTATTGTACGGCATTTAC	44	105	100	>200	>200	2	4
gs001212	pm1234	6,20	GCATTAAACAGGAAACAATA	CTGTCCATGTGGCATAAACC	44	110	110	105	107	1	1
gs001312	pm0606	7,18	AGATGCTAACATTAGGGATA	TTTTAGACATACAGAGGAGT	43	81	81	102	-	1	1
gs001441	pm1253	9,11	CCAGACTACAGGCTGATGGC	CCCTTACCCCAGCAACTCTT	55	75,130	75	>200	>200	1	1
gs001357	pm0115	9,M	ACCAATGTCACTGCTTCTAAAATA	CCCATAATAAGTGAAGAGGTAGTTC	48	125,155	127	125	>200	1	1
gs001261	pm0428	10,15,22	AAGAAATTGTTTACTGGATT	TTATCTGACTTGGAGGAAAT	42	107	107	-	-	1	1
gs001456	pm2420	10,15,22	ACTACCCCTGAGATATTAGTT	TTCATTTATTTGATTAGTTGA	46	100	100	170	-	1	1
gs000250	pm2303	11,M	ATACCACTTCCGCTGTCACG	GAGGAGCGTCTACTGGTCTT	50	72	74	72	>200	3	20
gs000314	pm2643	12,19	GCACCAAGAAGCAGTTCCAG	TTGGGAATGAGAAAATAACT	46	83	83	81	-	1	7
gs000403	pm2773	12,M	GATCTCAGTTCTGCGTTTATT	TACATACAAAGATGCAAACAGT	44	80	80	79	68	1	1
gs001487	pm2725	13,16	ATTCTTGTGTGCTGCTTTCC	GTCTCTCTTCTGATGGCTGA	46	62	60	135	180	1	1
gs000976	pm2780	14,16	AACCTGTTTTACCGCATCTT	AGGTTATTTGTCCACCAGAA	48	87	87	>200	>200	1	1
gs001435	pm1683	17,20,C	TGTTGGTTCACCATTGAGAC	AGAACAACACATCAAAGATGC	46	90	90	>200	90	1	1
gs001393	pm1748	17,22,Y	GAATGTCATCCAAGACGTAG	CTAGTTATATCCTGGCTCTG	44	81	81	>200	200	1	1
gs000056	pm0964	17,C	TTTATCCCAGCAAGCACAAC	TCTTCCTCTTCACTCTCCTC	49	120	120	>200	170	4	11
gs001369	pm2217	17,C	ACTTAAAGTAGCTTTGTACG	TGCCTCCTGGTCTGATAATA	43	95	95	>200	95	1	1
gs001440	pm1213	18,C	CCCCAGTTAAAGATTATTGT	AGTGACGATGGAAGGATGTA	44	92	92	-	92	1	1
gs001217	pm1118	19,20	TGCAGAGTGATTTTCCAGAG	CGTAGGTCATTCTTTTCAGC	46	75	72	160	65	1	1
gs001009	pm2824	19,22	ATCCCTCTGTCTATTCACAC	GCTCGTTTAACTCACTTCAC	46	110	110	130	170	2	2
gs001172	pm0887	19,22	GCCTGCATCTGTGTTGACTT	AACCTCTGGGAACAAATCAT	48	91	89	160	86	1	1

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Fig. 10

gi|1057	pm2049	C	AGGACACAAACACCAGCTAT	TTTTCTGATTATGACATGAC	45	75	75	101	75	1	1
gi|4773	pm1753	N	ATCTCTTTGTAGCCATCCTG	GTTAAAGTGCTGATGCCATT	42	64,100	64	64	>200	1	1
gi|1096	pm2236	N	GTAGAGCTGCATTGACTACC	ACAGACAAGGAATAATCATA	42	100,96	110	110	112	1	1
gi|1166	pm0506	N	GTCCCACAGTCCAGCCTAAC	GCCACATATTAGAATCCATC	46	74	74	74	>200	1	1
gi|1454	pm2354	N	TGTCTTTGTGGACTCTGCCT	TTTAACAGTCAATAAATACATGTT	44	110	110	110	106	1	1
gi|4029	pm2492	M.C	GCTAGAAAGAAGGGCACTCA	CTTAACTCGATAGCCAGGTC	46	75	75	75	75	1	1
gi|4253	pm2786	M.C	CACAAAACAGCAAACTTCAG	ATGGTTATTTTATCAGATTG	41	83	83	82	83	2	3
gi|4285	pm1704	M.C	TCCACCCAGAGAAGCACACT	AATTCATAGGGAATAGGTTC	40	75,130	75	75	75	1	23
gi|4302	pm2318	M.C	TCGAGAAGGACAAAATCACC	GAACAGGGTTAGTCCATTCG	48	58	58	58	58	1	1
gi|4543	pm1689	M.C	CATGAGGCTACGGAAACAGG	AGGAGTCCGTGGGTCTTGAG	51	84	84	84	84	4	18
gi|6675	pm1442	M.C	AAAGCATCTTGAGAGGAACA	GGAGGACTCGCTTGGTCTTA	49	110,>200	110	110	110	1	9
gi|7732	pm1452	M.C	GCAGCAGATACCTTTACACC	TGGTTCATTTCAGTTCCTTC	51	102	105	102	102	3	13
gi|8995	pm0268	M.C	GAAGCTCTTGTGAGGAAAGT	CAGACCCCATCTTTTATACC	47	79	79	79	79	3	4
gi|1016	pm2783	M.C	ACGATATTTATAGTGATGTG	TCAAAACTTTATATATGCT	40	93	93	91	92	1	1
gi|1053	pm1144	M.C	AGATGAGTGTGGGTCAGAGA	CCATTCCTGTCATTCCAGTT	52	135	140	135	135	1	1
gi|1127	pm2290	M.C	ACTGGTGATGGAAGGTTACA	CCACACAGTGAGCACCGTCT	47	55	55	55	55	1	1
gi|1167	pm1626	M.C	GAGAGCCCTTGCATCCTTTA	CTTCCCTTTGGTCTTTCTGT	49	100	100	100	100	1	1
gi|1216	pm2109	M.C	TAGTCAGAGATTCAGTAAGT	ACATGTATTTTGATAGTCTT	42	110	110	110	110	1	2
gi|1253	pm1240	M.C	AACTGGTTCCATCAAGACTG	AGTGAATAAACTCTCCACTCC	48	120	120	120	120	1	1
gi|1281	pm1131	M.C	ACTTAAAAACCCACCAGCAT	ACAACAGCAGTCAAATAGAA	47	97	97	97	97	1	1
gi|1375	pm0952	M.C	AAGAGGAGTTTCCCTGCTCA	ATCATGGCAGATGGCAAGGA	51	89	89	89	150	1	1
gi|1396	pm2216	M.C	ATCTGCATGACCTATAATCT	CGTTCTCTTTTATTTGACAT	45	108	108	108	108	1	1
gi|1411	pm0958	M.C	ATGGGTTTATCAGGGGTTTC	GAGACCAAAGGCACTTCTTA	47	80	77	80	80	1	1
gi|1460	pm2626	M.C	ACATTGAATGGGGATGAGGT	GGACATTTCTAGCCCCAGAGC	51	75,55	75	75	75	1	2
gi|1482	pm1210	M.C	TTGTTGACATTCCTTTTAGAA	CAGTGCCTCTGTACTGAGACA	46	85	85	85	85	1	2
gi|1490	pm0109	M.C	GCCCACAGAGACATCATCCT	TCTTAGTAGGTGCTCTGGTG	51	98	98	98	98	1	1
gi|6188	pm2042	No product	CAACCAGTTAGCGTGAAAGT	GAAATAATCCTTGTCATCTA	45	87	87	-	-	1	1
gi|8850	pm0304	No product	CTTTGGGATATTTTCTTCAT	CCCTCGGGTACTTTTCTATG	43	60	60	62	-	1	2
gi|9983	pm0808	No product	AGCCAGCCTCTTTGTATGTG	CTGGATTTGATTTTCATTAG	44	87	87	-	112	1	1
gi|1254	pm1671	No product	TGTGGTATGAAAATATCTGA	TTATGAATGAAGACAACACT	43	90	90	103	>200	1	1
gi|1365	pm2908	No product	CAGTAGTGTGCTTTGAAATG	TTTATGTGAAATGTGGTTGT	41	63	63	-	150	3	3
gi|1373	pm0361	No product	TACAGCCGGCTTCTAAAAGTC	TTTGAGCATCAAGGAAATCT	46	82	82	-	>200	1	1
gi|1556	pm0849	No product	TACATTCTTCAGACTCATCG	TTTTCAAAAACTTTATTCTT	40	86	86	>200	100	1	1
gi|1574	pm1284	No product	ATCAGAGCTCAGTTCCTGTAG	ATTTTGCCTCTTGCATGGTC	44	57	57	67	67	2	2
gi|1622	pm1606	No product	GATCTTGAGCCTTAACTGGA	TTTGCAGTTCAGCTTTATTC	45	54	54	-	-	1	1
gi|1640	pm0852	No product	GATCTCTGTTCCTTTTCACA	TTTATAACAAGACACCATAC	36	45	45	-	-	1	1

Fig. 11

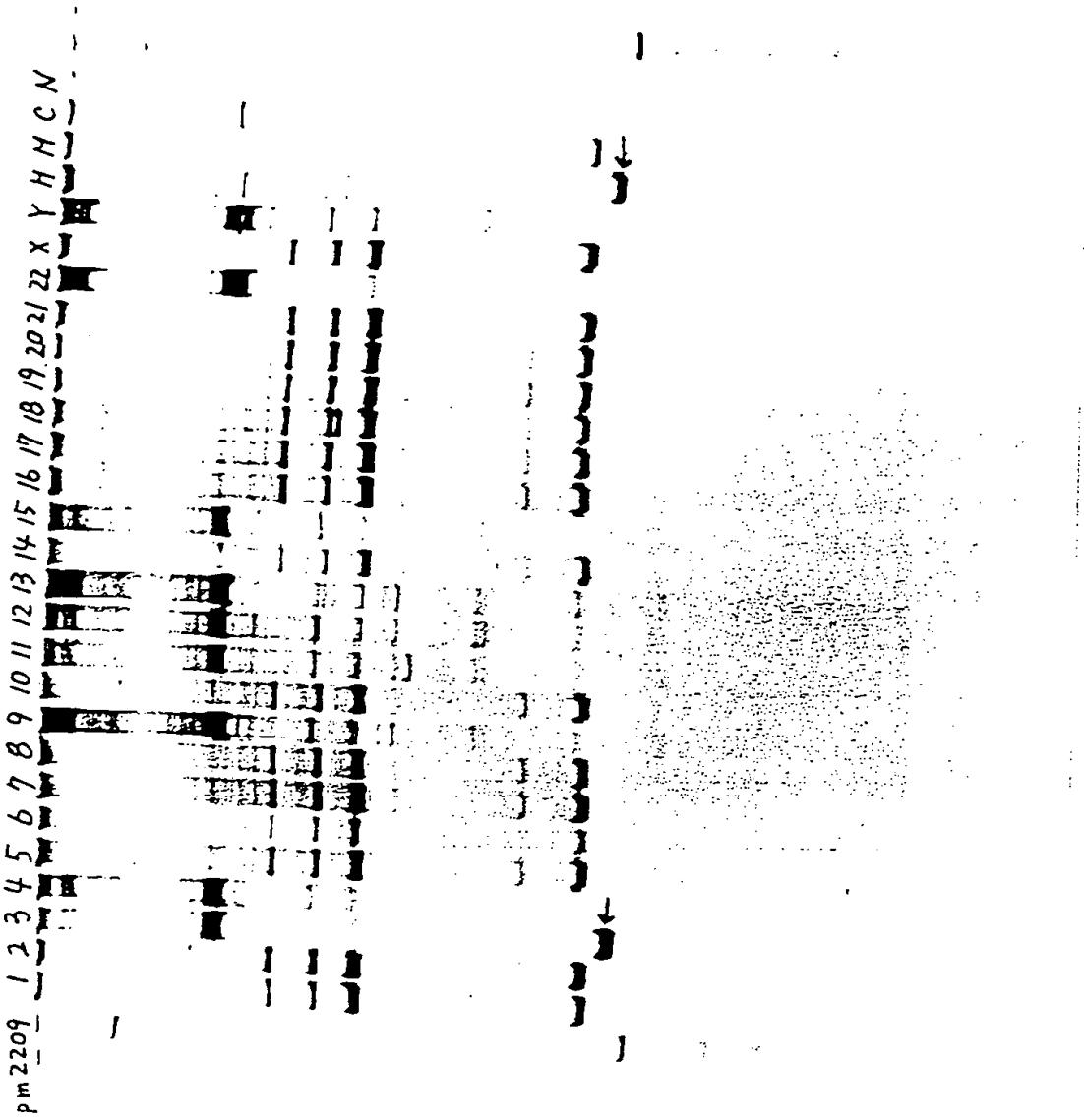

Fig. 12

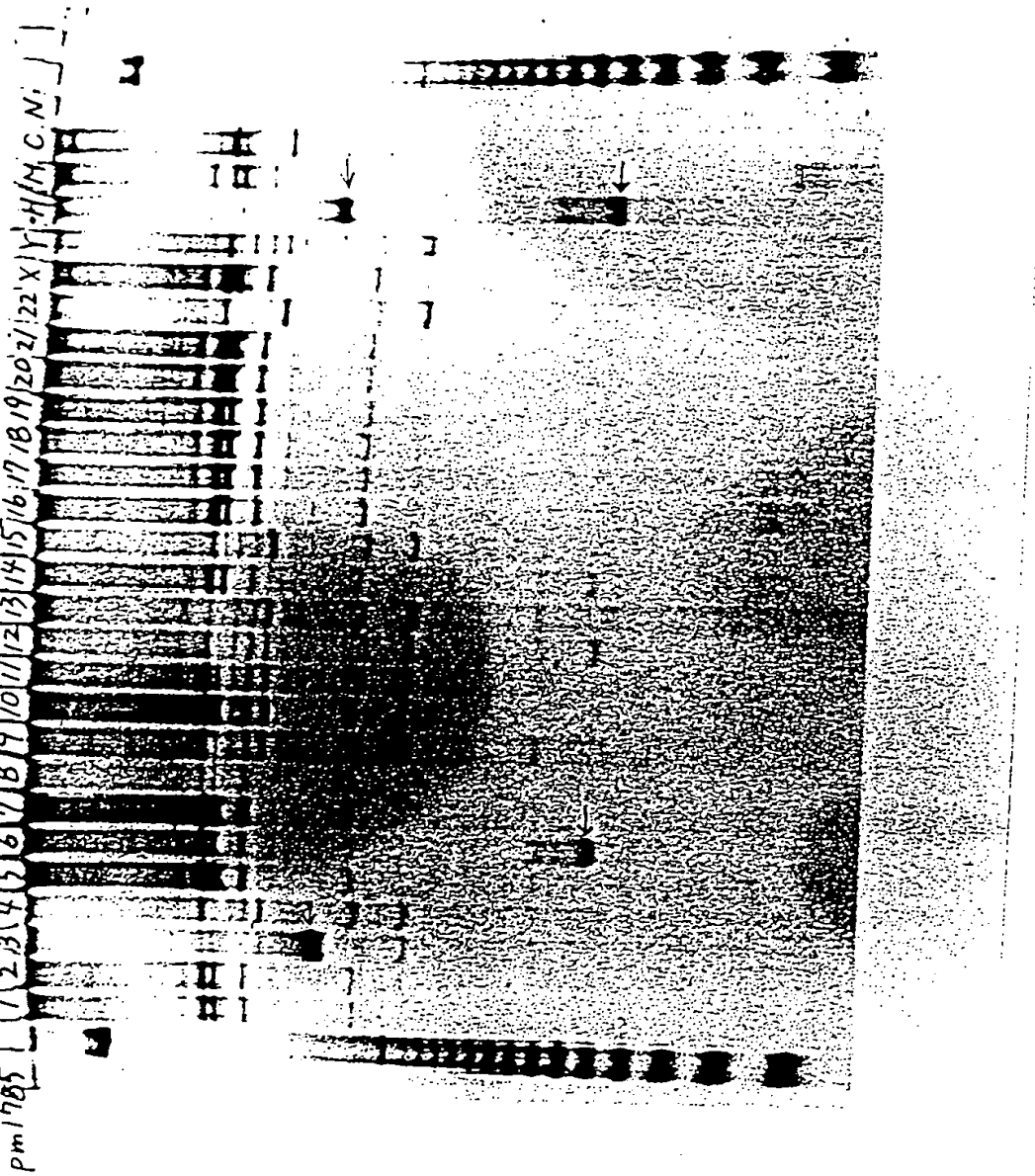

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Fig. 13

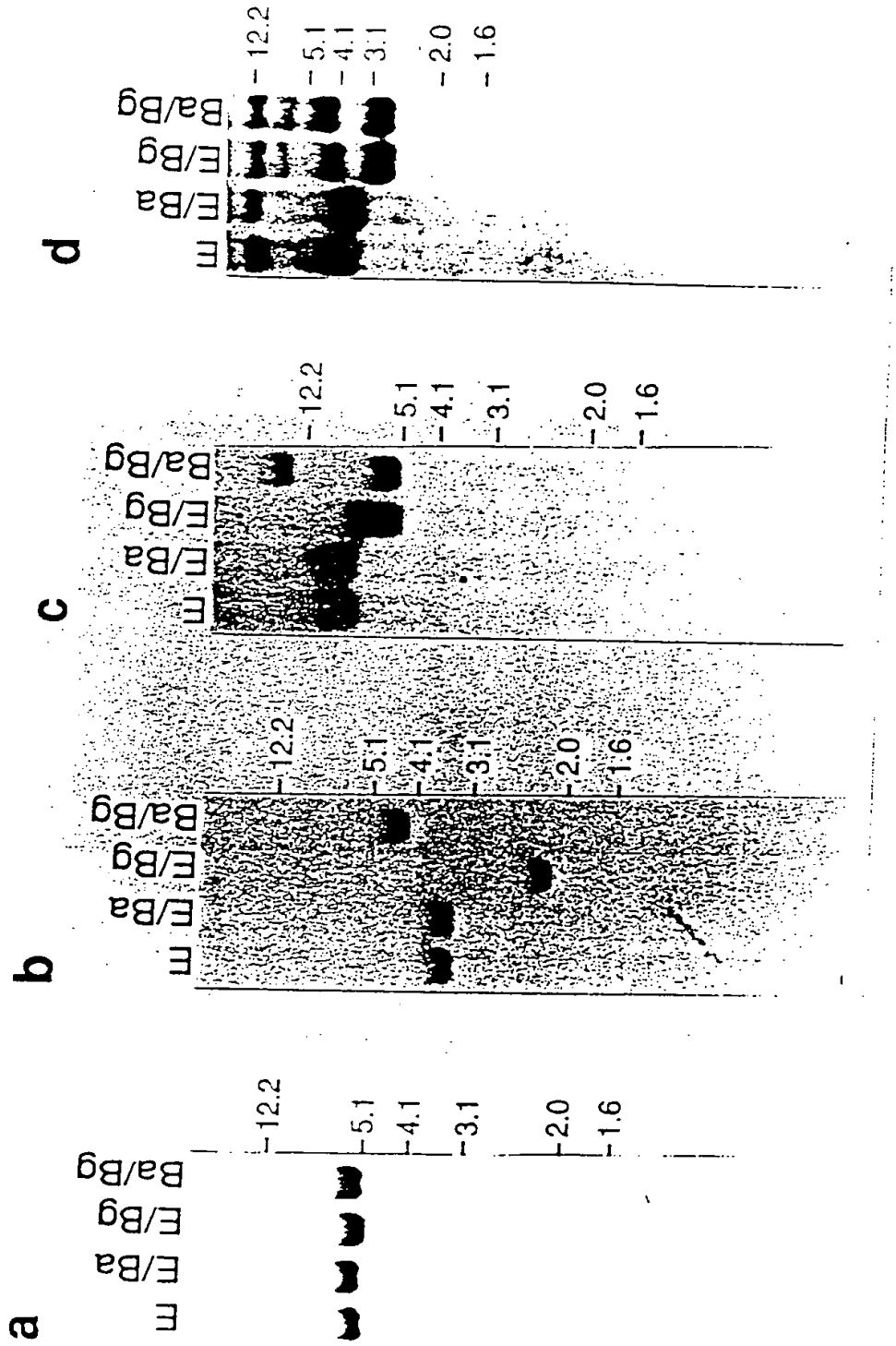

Fig. 14

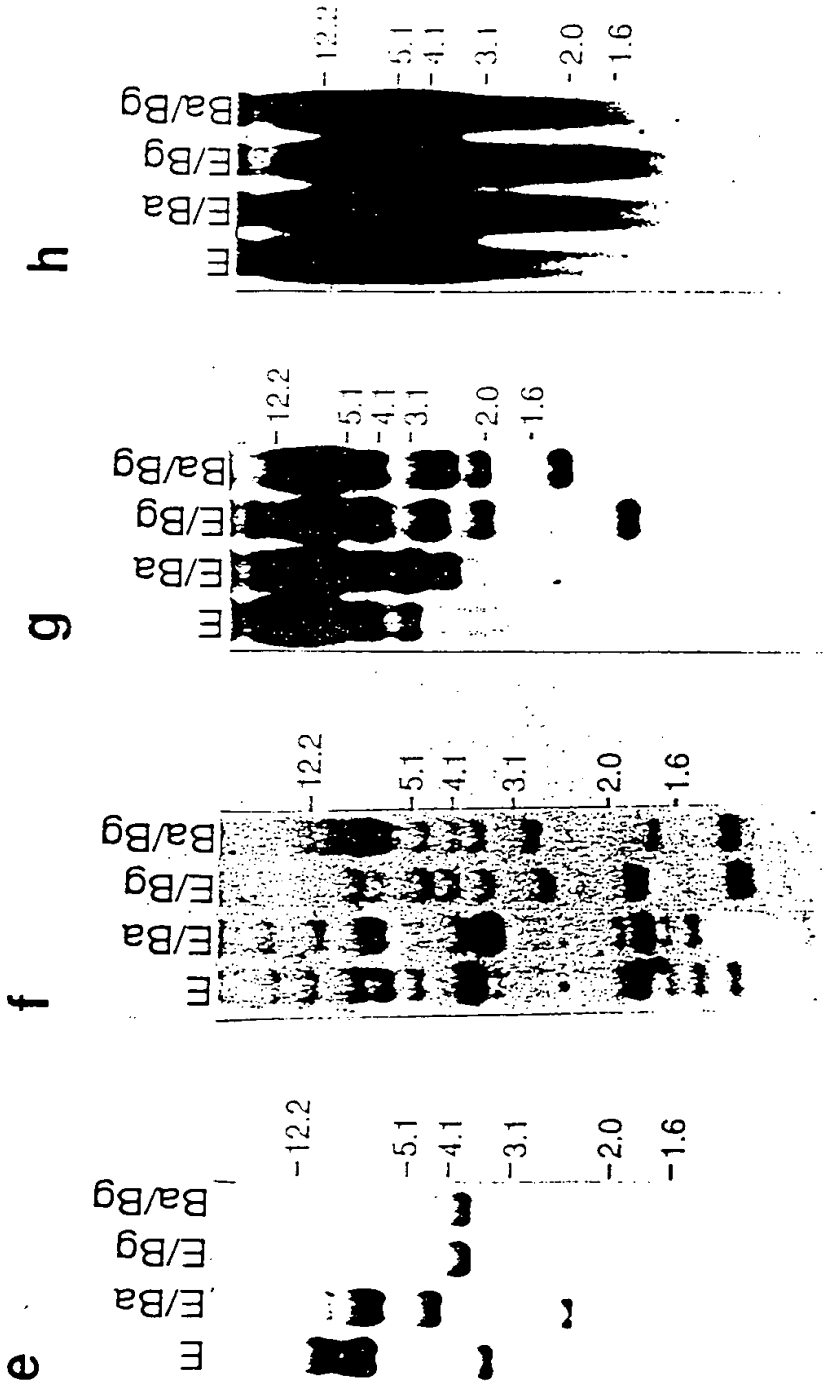

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Fig. 15

Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (8)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A *	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868 *	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418 *	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10498	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9

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Fig. 16

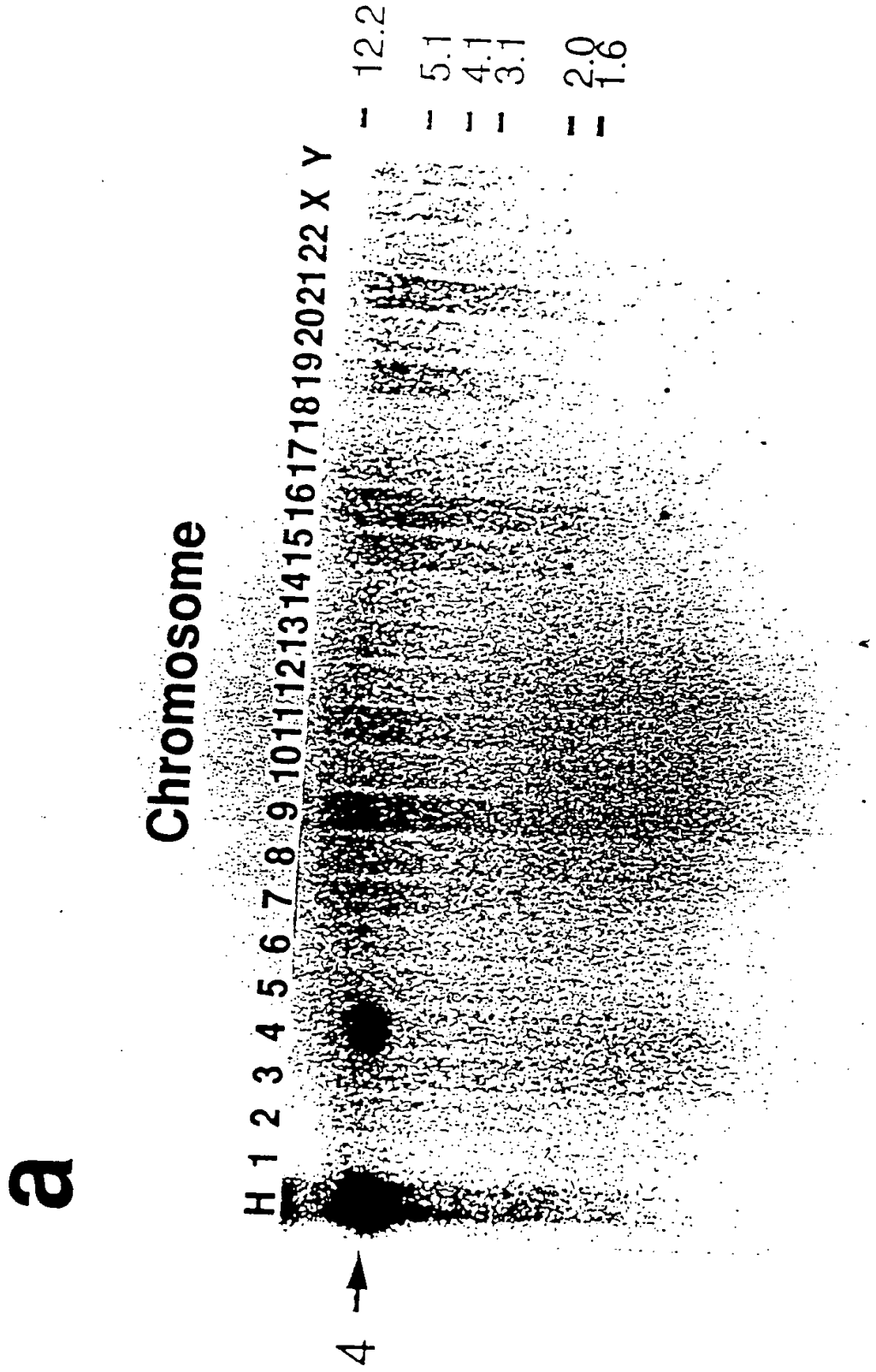

Fig. 17

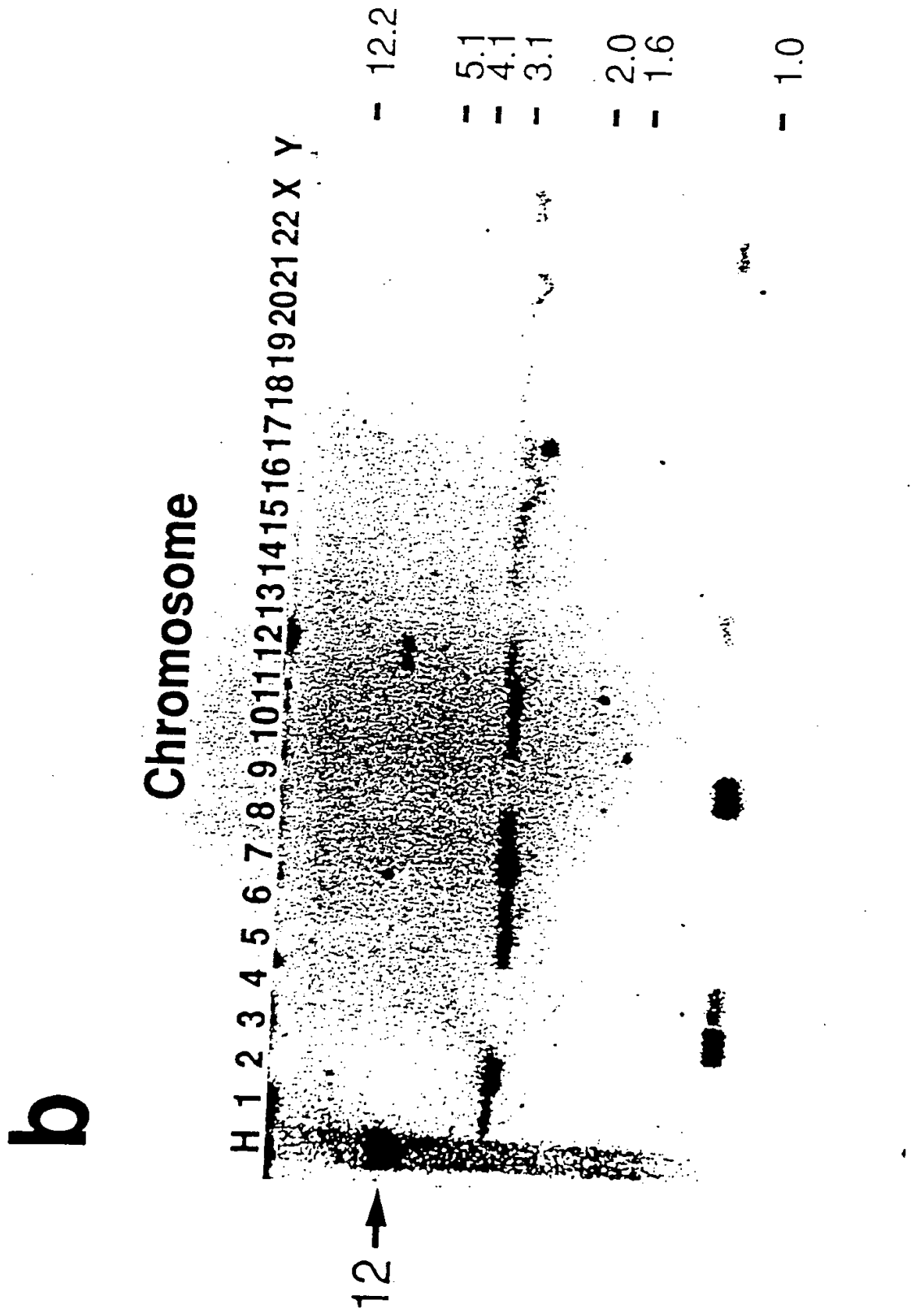
b
Chromosome
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
12.2
5.1
4.1
3.1
2.0
1.6
1.0
12

Fig. 18

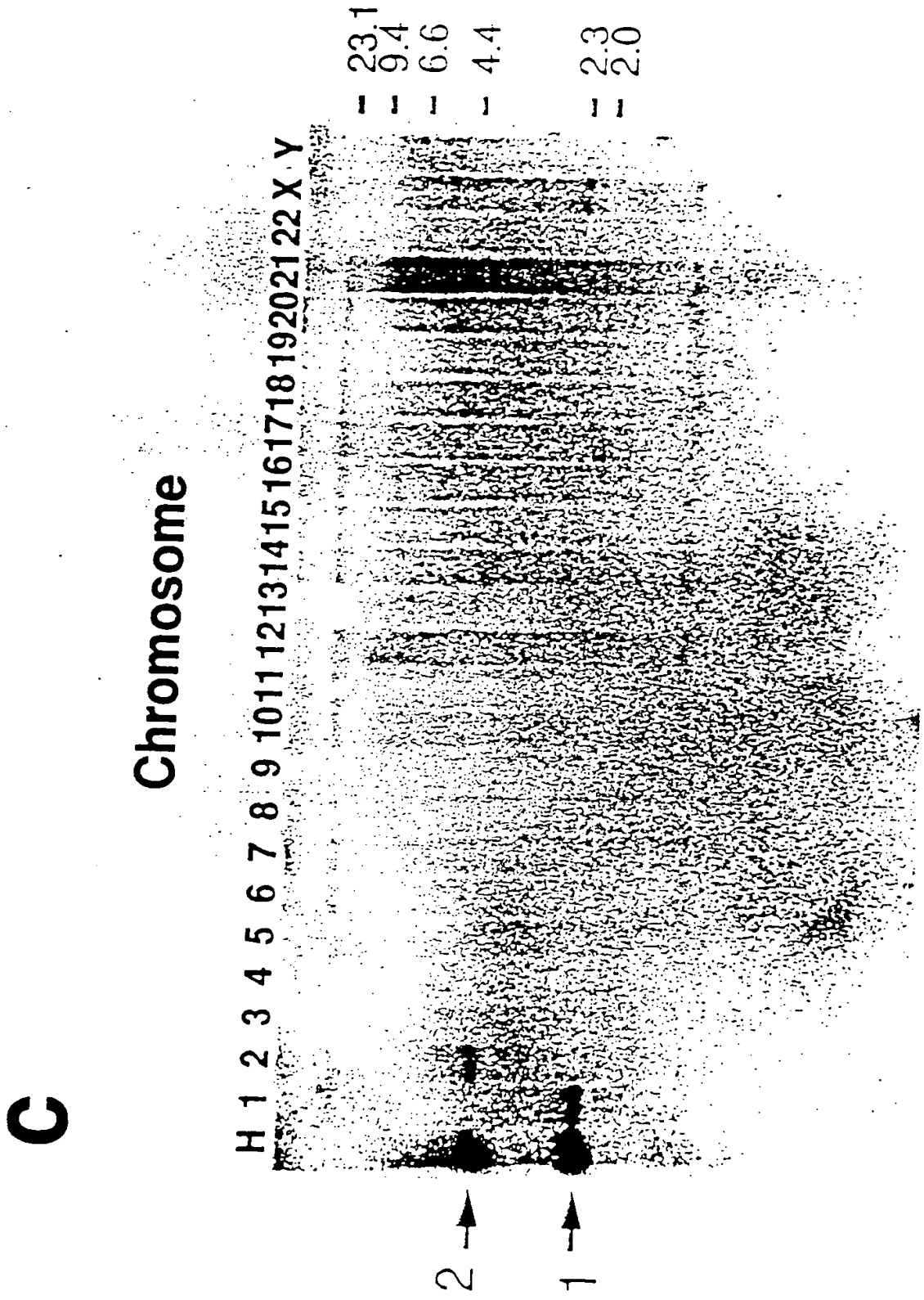
C
Chromosome
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
23.1
9.4
6.6
4.4
2.3
2.0
2
1

Fig. 19

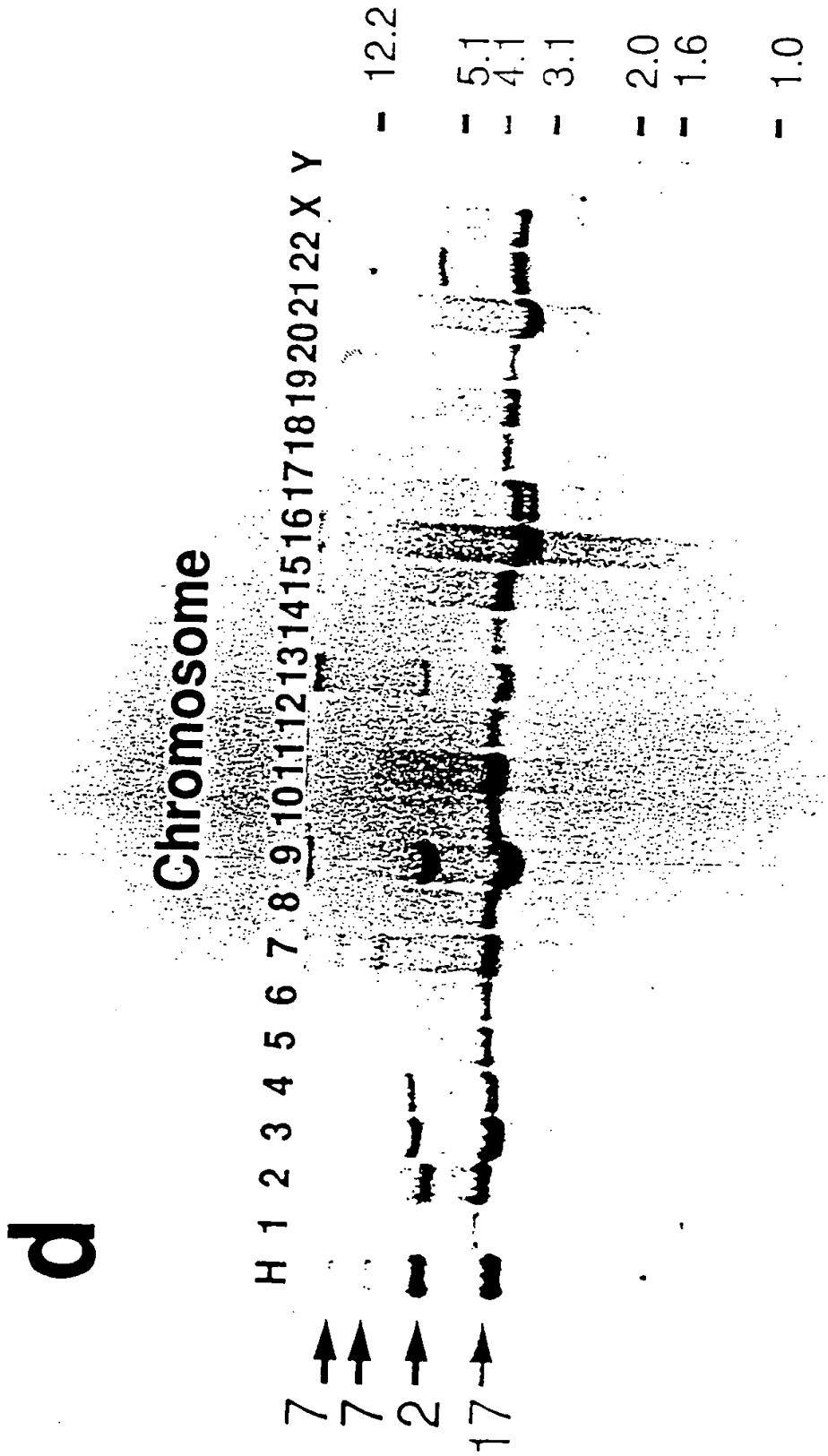
d
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
Chromosome
12.2
5.1
4.1
3.1
2.0
1.6
1.0
7
7
2
17

Fig. 20

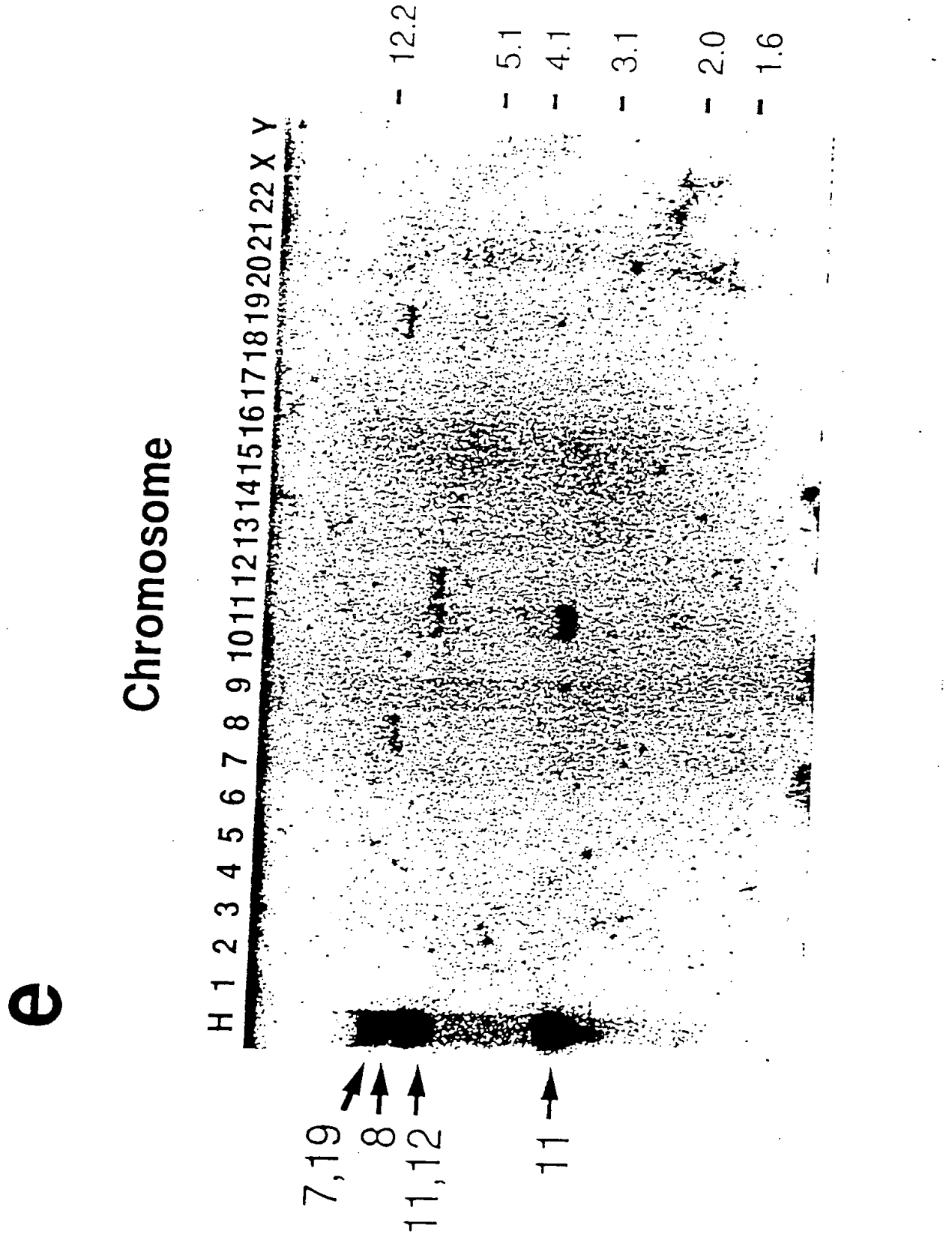
e
Chromosome
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
12.2
5.1
4.1
3.1
2.0
1.6
7,19
8
11,12
11

Fig. 21

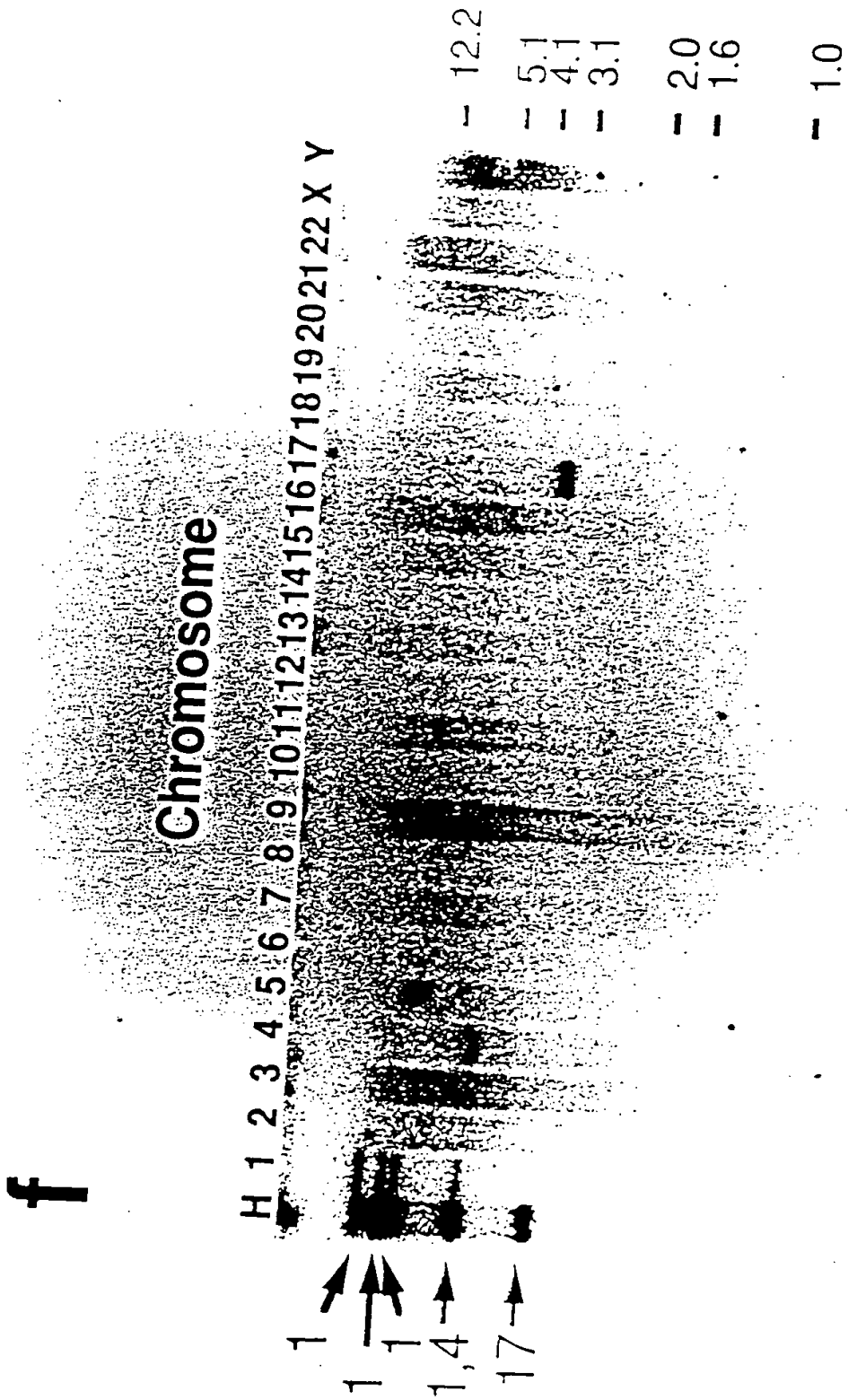
f
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
Chromosome
12.2
5.1
4.1
3.1
2.0
1.6
1.0
1
1
1,4
17

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Fig. 22

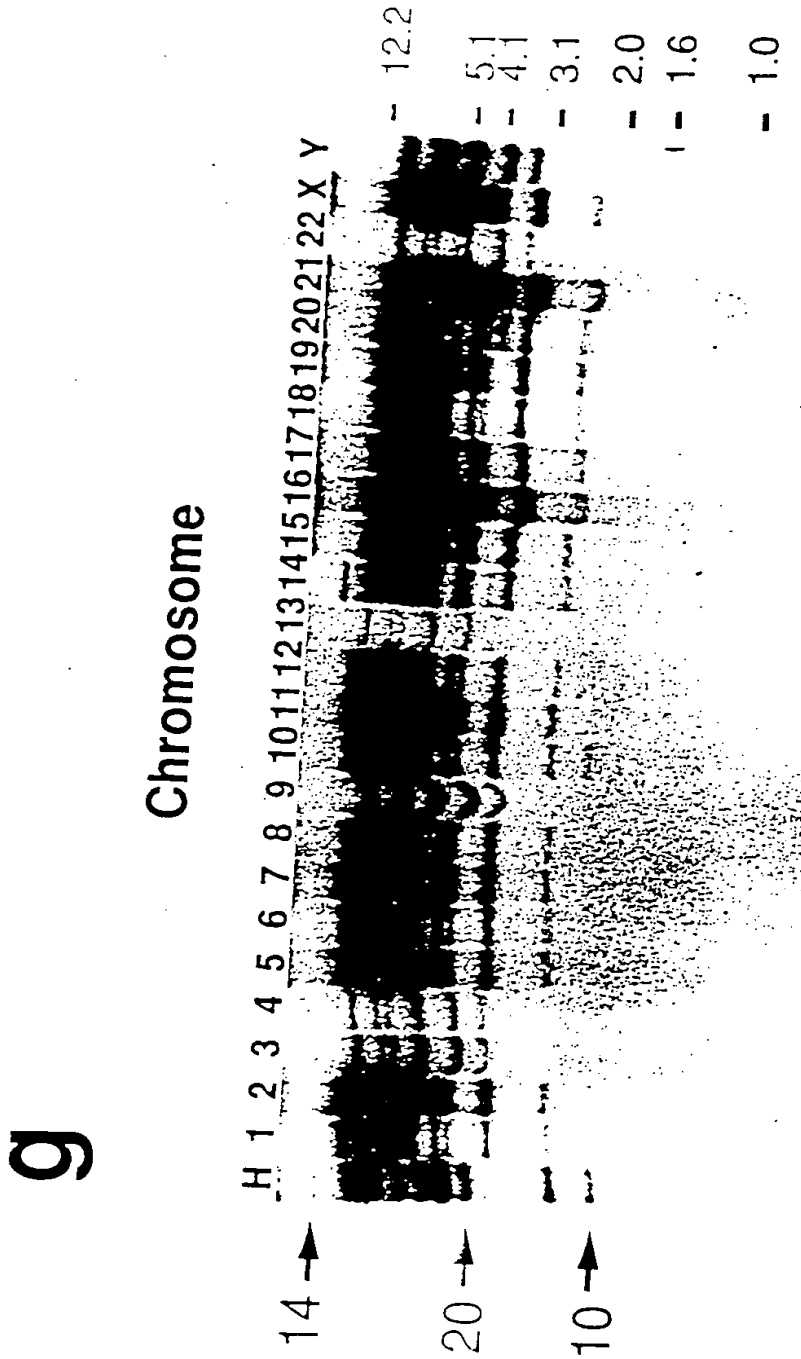

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Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Clone		Sequence length	Numbers of bands detected with human whole chromosomes: E	E/Ba	E/Bg	Ba/Bg	Chromosomes assigned	Background: Mouse	Background: Chinese hamster
Single band group:									
c12c11	GS000075	432	1	1	1	1	9	0	0
c12c06	GS000062	540	1	1	1	1	6,15	0	0
c12g01	GS000280	212	1	1	1	1	2	1	1
c13c05	GS000117	359	1	1	1	1	11+	0	0
c13c07	GS000120	355	1	1	1	1	2	0	0
c13f10	GS000206	267	1	1	1	1	14	0	0
c13h01	GS000279	183	1	1	1	1	12+	0	0
c13h02	GS000322	167	1	1	1	1	6	0	0
d0g02	GS000095	397	1	1	1	1	3	0	0
d0h07	GS000164	313	1	1	1	1	11	1	1
d1b10	GS000348	153	1	1	1	1	20	0	0
hm01a12	GS000223	246	1	1	1	1	Y?	0	0
hm01e09	GS000423	157	0	1	1	1	1	0	0
hm01e12	junk	394	1	1	1	1	17	0	0
hm01f05	GS000066	454	1	1	1	1	19,22	0	0
hm01f10	GS000299	173	0	1	1	1	10	0	0
hm01g09	GS000053	477	1	1	1	1	6	0	0
hm01h07	GS000115	368	1	1	1	1	12	0	0
hm02a02	GS000130	344	1	1	1	1	4	0	0
hm02a04	GS000329	164	1	1	0	0	10	0	0
hm02c01	GS000203	271	1	1	1	1	15	0	0
hm02c01	GS000015	590	1	1	1	1	20	0	0
hm02e02	GS000342	156	0	1	1	1	14	0	0
hm02e05	GS000401	223	1	1	0	0	n.d.	0	0
hm02g02	GS000191	278	1	1	1	1	17	0	0
hm05a05	GS000251	219	1	1	1	1	6	2	0
hm05a10	junk	392	1	1	1	1	1	1	1
hm05e10	GS000009	606	1	1	1	1	1	0	0
kmd01	junk	169	1	1	1	0	n.d.	0	0
s105	GS000001	703	1	1	1	1	5	0	0
s110	GS000057	471	1	1	1	1	8	0	0
s11d11	GS000307	#175	0	0	0	1	7	0	0
s11h01	GS000269	204	1	1	1	1	3	0	0
s147	GS000060	461	1	1	1	0	2	0	0
s14e06	junk	639	1	1	1	1	1	0	0
s14g02	GS000152	322	1	1	1	1	4	0	0
s14h12	GS000271	193	1	1	1	1	4	1	1
s150	GS000143	330	1	1	1	1	17	0	0
s156	GS000002	306	1	1	1	1	2	1	1
s15b11	GS000250	221	1	1	1	1	14	0	0
s179	GS000275	196	1	1	1	1	n.d.	0	0
s246	GS000234	241	1	1	1	1	9	0	0
s247	GS000247	153	1	1	1	1	1	0	0
s270	junk	135	1	1	1	1	19	0	0

Fig. 24

Clone		Sequence length	Numbers of bands detected with human whole chromosomes: E	E/Bα	E/Bβ	Bα/Bβ	Chromosomes assigned	Background: Mouse	Chinese hamster
s306	GS000256	205	1	1	0	1	X	0	0
s309	GS000171	305	1	1	0	1	1	0	0
s342	GS000323	165	1	1	1	1	4	3	2
s331	GS000265	207	1	1	0	1	6,15	1	1
s334	GS000165	312	1	1	1	1	1	0	0
s337	GS000276	195	1	1	1	1	17	0	0
s339	GS000295	180	1	1	1	1	n.d.	0	1
s443	GS000330	251	1	1	1	1	n.d.	0	0
s470	junk	261	1	1	1	1	17	0	0
s474	GS000192	278	1	1	1	1	5	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	GS000334	161	1	1	1	1	14	1	1
s632	junk	587	1	1	1	1	2	0	0
s633	GS000166	311	1	1	1	1	22	2	1
s650	GS000041	644	1	1	1	1	12	1	1
tw1-04	GS000025	537	1	1	1	1	3,7	0	0
tw1-19	GS000218	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	GS000237	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	8	1	1
tw1-48	GS000098	173	1	1	1	1	14	0	0
tw1-96	GS000133	339	1	1	1	1	11	0	0
Two band group :									
c12f12	GS000195	277	1	2	2	2	1,	1	1
c13d02	GS000042	503	2	2	1	1	2,	0	0
hm01a06	GS000129	344	2	2	2	2	11,18	3	5
hm01a07	GS000207	269	2	2	2	2	7,	0	0
hm01d05	GS000232	243	2	2	2	1	2,	0	0
hm01e01	GS000181	292	2	2	2	2	1,2	0	0
hm02a08	GS000435	302	2	2	2	2	3,	1	1
hm02c04	GS000221	253	2	2	2	2	3,	0	0
hm02c05	GS000146	332	2	2	2	2	17,19,22	0	0
hm05f07	GS000043	503	1	1	2	1	3,	0	0
s11d06	GS000268	205	2	2	2	2	11,12	0	0
s11g12	GS000337	255	2	2	2	2	6,	0	0
s124	GS000083	404	2	2	2	2	9,	1	1
s144	GS000132	342	1	2	2	2	1,7	0	0
s14f03	GS000239	243	1	2	2	2	2,	3	2
s15e02	junk	439	2	2	1	2	6,	0	0
s16b09	junk	420	1	1	1	2	10,14	0	0
s17c09	GS000248	223	2	2	2	2	14,	0	0
s231	junk	284	2	2	2	2	11,	0	0
s254	GS000124	353	2	2	2	2	1,	3	1
s255	GS000235	239	2	2	2	2	11,	0	0
s272	junk	195	2	2	2	2	10,16	1	1

Fig. 25

Clone	Sequence length		Numbers of bands detected with human whole chromosomes: E	E/Ba	E/Bg	Ba/Bg	Chromosomes assigned	Background: Mouse	Chinese hamster
s311	GS000092	333	1	1	2	2	16.	1	1
s313	junk	132	2	2	1	0	20.	0	0
s317	GS000100	339	0	0	1	2	14,14	1	1
s336	GS000134	337	2	2	2	2	12,14	0	0
s338	GS000139	283	2	2	2	1	22,X	0	0
s339	GS000233	187	2	1	1	2	17.	0	0.
s394	GS000068	449	2	1	2	2	13,14	0	0
s396	junk	277	2	2	2	2	17.	0	1
s455	junk	452	1	2	2	1	4.	0	0
s456	GS000286	132	2	2	2	2	8,10	1	2
s465	GS000201	274	1	1	2	2	6,15	0	0
s635	junk	260	1	1	1	2	9,13	0	0
s639	GS000287	205	1	2	2	2	2,X	0	0
s656	GS000025	#590	2	2	0	2	6,11	0	0
tw1-33	junk	352	2	2	2	2	1.	0	0
tw1-39	GS000153	#321	2	2	2	2	17.	0	0
tw1-70	GS000061	441	1	1	2	1	11.	0	0
tw1-80	junk	453	2	2	1	2	9,17	2	2
tw1-87	GS000158	316	2	2	2	2	7.	0	0
Three band group									
d0h06	GS000080	417	3	3	3	1	1.	0	0
hm05b07	junk	386	2	3	3	3	5.	0	0.
hm05g02	GS000209	267	2	2	2	1	3,17,19	1	1
s129	GS000107	378	3	3	3	3	n.d.	1	1
s178	GS000357	146	1	2	2	3	2.	0	0
s17a10	GS000294	181	3	3	3	3	2,13,22	1	1
s308	GS000412	688	2	2	2	3	XX	1	1
s401	GS000224	249	2	3	3	3	6,6.	0	0
s654	GS000045	491	3	3	3	3	1,22.	0	0
tw1-82	GS000208	267	3	3	3	3	13.	4	0
Four band group									
c12g07	GS000154	320	4	4	2	3	5, 14.	0	0
c13a08	GS000055	508	3	3	4	4	2,7,7,17	1	2
c13c04	GS000106	#376	4	3	3	3	n.d.	0	2
c13e09	GS000302	195	4	2	4	4	2,17.	7	2
s136	GS000160	315	4	4	4	4	4,X.	2	1
s163	GS000004	#618	4	4	4	2	4,4,8,20	3	1
s479	GS000130	293	4	4	2	2	7,8,11,11,12,19	0	0
Group with 5 or more bands									
c12f08	GS000253	217	5	5	5	2	2,7,9,14.	2	0
hc01	junk	374	12	12	15	13	1,2,6.	22	20
hd10	junk	361	4	4	4	8	n.d.	12	6
he10	junk	178	6	2	3	3	6,8,9,19,21.	3	3
hm01c05	GS000305	176	9	7	5	5	X.	9	8
hm01f04	GS000246	215	8	10	5	5	n.d.	12	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14	6

Fig. 26

Clone		Sequence length	Numbers of bands detected with human whole chromosomes: E	E/Ba	E/Bg	Ba/Bg	Chromosomes assigned	Background: Mouse	Chinese hamster
hm02f09	GS000273	442	8	7	7	5	3,3,6,11,13,14,15,16	0	0
hm05a02	GS000096	373	5	6	4	6	2,8,17,	3	3
hm05a04	GS000236	#239	6	6	6	7	n.d.	8	5
kmb01	junk	350	3	5	5	5	13,	14	7
s11f06	GS000316	170	6	6	6	4	1,2,2,3,4,6,13,15,	0	3
s14f01	GS000407	262	12	11	10	9	1,6,9,13,	6	3
s173	GS000094	397	5	4	6	8	1,1,1,1,4,17	0	0
s265	GS000323	167	10	12	11	14	18,	9	5
s341	junk	494	9	9	8	6	n.d.	15	8
s406	GS000113	364	6	7	5	4	2,7,8,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,2,6,11,X,	3	5
tw1-63	junk	203	8	10	10	12	3,4,	17	11
Bands no detected:									
e13g02	GS000340	157	0	0	0	0	-	-	-
hm01e10	junk	232	0	0	0	0	-	-	-
hm02d11	GS000274	196	0	0	0	0	-	-	-
s323	GS000278	194	0	0	0	0	-	-	-
s359	GS000199	279	0	0	0	0	-	-	-
s511	junk	233	0	0	0	0	-	-	-
s645	GS000012	#734	0	0	0	0	-	-	-
s647	GS000105	360	0	0	0	0	-	-	-
s651	junk	540	0	0	0	0	-	-	-